

Appl. No. : 09/509,234
Filed : September 25, 2000

- ATGCATATTTCCGTAA (SEQ ID NO: 33)
- CAGCAGATGACATCATT (SEQ ID NO: 34)
- CATCTAAAGATATATTAAATGGA (SEQ ID NO: 35)
- AGTATTAGCAAATGCGGGTCAC (SEQ ID NO: 36)
- CAACACAACTCAATTAGAA (SEQ ID NO: 37).

Please amend the paragraph beginning on page 17, line 25 as follows:

In order to purify bacterial DNA, 200 μ l of supernatent were then filtered on a Macherey-Nagel Nucleospin C+T[®] column and eluted with 200 μ l sterile H₂O. Two different amounts of DNA suspension (2 μ l and 200 μ l) were submitted to multiplex PCR amplification with the primers 5'-TGGCTATCGTGTACAATCG-3' (SEQ ID NO: 38) and 5'-CTGGAACCTGTTGAGCAGAG-3' (SEQ ID NO: 39) for *mecA* and the above-described primers for *femA*, yielding different fragments.

IN THE CLAIMS:

Please cancel Claims 6, 11, 15-23, 31, 32, and 34-42.

Please amend the following claims:

1. (Twice Amended) An isolated or purified oligonucleotide for the specific identification of *Staphylococci* species, comprising a nucleotide sequence of about 25 to 350 base pairs of the "consensus" *femA* nucleotide sequence SEQ ID NO:1.
2. (Twice Amended) The oligonucleotide according to claim 1 comprising a nucleotide sequence of about 25 to 250 base pairs of SEQ ID NO:1.
5. (Twice Amended) The oligonucleotide according to claim 1, wherein the nucleotide sequence comprises about 25 to 45 base pairs.
7. (Three Times Amended) Two or more isolated or purified oligonucleotides for the specific amplification of *Staphylococci* species comprising at least one nucleotide sequence of about 25 to 45 base pairs more than 60% homologous to SEQ ID NO:1 or at least one oligonucleotide about 25 to 45 base pairs more than 60% homologous to SEQ ID NOS:1 and 29-37.
8. (Twice Amended) The oligonucleotides according to Claim 7 wherein said oligonucleotides have more than 70% homology to SEQ ID NOS:1 and 29-37.

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9. (Twice Amended) The oligonucleotides according to Claim 8 wherein said oligonucleotides have more than 80% homology to SEQ ID NOS:1 and 29-37.

10. (Twice Amended) The oligonucleotides according to Claim 9 wherein said oligonucleotides have more than 90% homology to SEQ ID NOS:1 and 29-37.

13. (Twice Amended) A method of identification and/or quantification of a *Staphylococci* species, which may present resistance to antibiotics and which is present in a sample, said method comprising the steps of:

obtaining a nucleotide sequence from a *Staphylococci* species present in the sample,

amplifying said nucleotide sequence with two or more isolated oligonucleotides for the specific amplification of *Staphylococci* species comprising at least one nucleotide sequence of about 15 to 45 base pairs more than 60% homologous to SEQ ID NO: 1 or at least one oligonucleotide about 15 to 45 base pairs more than 60% homologous to SEQ ID NOS: 1 and 29-37, and

identifying and/or quantifying the specific *Staphylococci* species:

by reverse hybridization of the amplified nucleotide sequence with one or more oligonucleotide(s) having a nucleotide sequence comprising about 15 to 350 base pairs of SEQ ID NO:1, specific of said *Staphylococci* species wherein said nucleotide sequence is immobilized on a solid support or

by a comparative measure of the length of the amplified nucleotide sequence.

14. (Twice Amended) A diagnostic device for the identification of *Staphylococci* species comprising: an oligonucleotide having a nucleotide sequence comprising about 15 to 350 base pairs of SEQ ID NO:1, or two or more isolated or purified oligonucleotides for the specific amplification of *Staphylococci* species comprising at least one nucleotide sequence of about 15 to 45 bases pairs more than 60% homologous to SEQ ID NO: 1 or at least one oligonucleotide about 15 to 45 base pairs more than 60% homologous to SEQ ID NOS: 1 and 29-37.

33. (Amended) The diagnostic device of Claim 14 further comprising reagents necessary for the identification of an amplified sequence of said *Staphylococci* species through any one of the methods selected from the group consisting of: *in situ* hybridization, hybridization on a solid support, hybridization in solution, hybridization on a dot blot, Northern blot, Southern

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blot, probe hybridization by the use of an isotopic label, probe hybridization by the use of a non-isotopic label, genetic amplification and a mixture thereof.

Please add the following claims:

43. (NEW) A method according to claim 13 wherein said oligonucleotides have more than 70% homology to SEQ ID NOS: 1, 46, 48, 50, and 52.

44. (NEW) A method according to claim 13 wherein said oligonucleotides have more than 80% homology to SEQ ID NOS: 1, 46, 48, 50, and 52.

45. (NEW) A method according to claim 13 wherein said oligonucleotides have more than 90% homology to SEQ ID NOS: 1, 46, 48, 50, and 52.

46. (NEW) A method according to claim 13 wherein said oligonucleotides are selected from the group consisting of SEQ ID NOS: 1, 18-40, 42, and 44.

47. (NEW) A diagnostic kit according to claim 14 wherein said oligonucleotides have more than 70% homology to SEQ ID NOS: 1, 46, 48, 50, and 52.

48. (NEW) A diagnostic kit according to claim 14 wherein said oligonucleotides have more than 80% homology to SEQ ID NOS: 1, 46, 48, 50, and 52.

49. (NEW) A diagnostic kit according to claim 14 wherein said oligonucleotides have more than 90% homology to SEQ ID NOS: 1, 46, 48, 50, and 52.

50. (NEW) A diagnostic kit according to claim 14 wherein said oligonucleotides are selected from the group consisting of SEQ ID NOS: 1, 18-40, 42, and 44.

REMARKS

The application has been amended to overcome objections to the specification and to more clearly claim the invention. No new matter is added herewith. Changes to the application can be seen on a separate page entitled VERSION WITH MARKINGS TO SHOW CHANGES MADE following the signature page. Deletions are in **[bold and brackets]** and insertions are underlined.

Objection to the Specification

The Examiner objected to the specification for not identifying SEQ ID NOS for sequences listed in the specification. Applicants have amended the specification to provide reference to SEQ ID NOS. Applicants respectfully request withdrawal of the objection on this basis.